

Exhibit A



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]

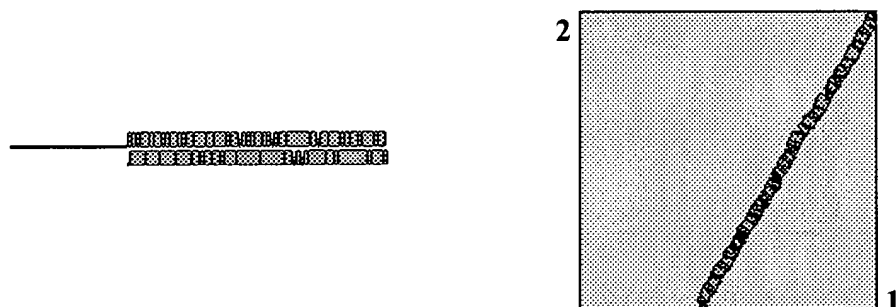
Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☐ View option: **Standard**
 Masking character option: **X for protein, n for nucleotide** Masking color option: **Black**
☐ Show CDS translation **Align**

Sequence 1: gi|47117817|sp|O75376|NCOR1_HUMAN Nuclear receptor corepressor 1 (N-CoR1) (N-CoR).

Length = 2440 (1 .. 2440) SEQ ID NO: 11

Sequence 2: gi|1045655|gb|AAC50236.1|silencing mediator of retinoid and thyroid hormone action

Length = 1495 (1 .. 1495) HSU37146



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 658 bits (1697), Expect = 0.0

Identities = 556/1576 (35%), Positives = 786/1576 (49%), Gaps = 234/1576 (14%)

Query	993	PCGTS--KSPNREWEVLQAPH----QVITNLPEGVRLP-----TTRPTRPPPPPLIPSSK	1041
		PC TS P EV++ +PH + P G LP T RP P PP I +	
Sbjct	25	PCWTSGLPFPVPPREVIKASPHAPDPSAFSYAPPGHPLPLGLHDTARPVLPRPPTISNPP	84
Query	1042	TTVASEKPSFIMG---GSISQGTPTGYLTSHNQASYTQETPKPSVGSISLGLPRQESAK	1098
		++S K ++ G+ISQG ++ Y++ P VG +++GLP + K	
Sbjct	85	PLISSAKHPSVLERQIGAISQG-----MSVQLHVPYSEHAKAP-VGPVTMGLPLPMDPKK	138
Query	1099	SATLPYIKQEEFSPRSQNSQPEGLLV-RAQHEGVVRGTA-GAIQEGSITRGTPPTSKISVE	1156
		A +KQE+ SPR Q PE L V AQ V+RGTA G++ GSIT+G P++++ +	
Sbjct	139	LAPFSGVKQEQLSPRGQAGPPESLGVPTAQEASVLRGTALGSVPGGSITKGIPSTRVPSD	198
Query	1157	SIPSLRGSITQGTTPALPQTGIPTALVKGSISRMPIEDSSP--EKGREEAASKGHVIYEG	1214
		S + RGSIT GTPA + L KG+I+R+ EDS ++GRE++ KGHVIYEG	

Sbjct	199	SAITYRGSITHGTPA-----DVLYKGTITRIIGEDSPSRLDRGREDSLPKGHVIYEG	250
Query	1215	KSGHILSYDNIKNA-----REGTRSPRTAHEISL-KRSYESVEGNIKQGMRESVPVSAP	1268
		K GH+LSY+ + +G S HE + KR+Y+ +EG + + +S SA	
Sbjct	251	KKGHVLSYEGGMSVTQCSKEDGRSSSGPPHETAAPKRITYDMMEGRVGRAIS-----SAS	304
Query	1269	LEGLICRALP--RGSPHSDLKERTVLSGSIMQGTTPRATTESFEDGLKYP-KQIKRES---	1322
		+EGL+ RA+P R SPH LKE+ + GSI QG PR+ E+ ED L+ K +KRE	
Sbjct	305	IEGLMGRAIPPERHSPHH-LKEQHHRGSITQGIIPRSYVEAQEDYLRREAKLLKREGTPP	363
Query	1323	--PPIRAFEGAIT-----KGKP-YDG-ITTIKEMGRSIEIIPRQDILTQESRKTPEVV	1371
		PP R A K KP ++G + T+KE GRSIHEIPR+++ R TPE+	
Sbjct	364	PPPPSRDLTEAYKTQALGPLKLKPAHEGLVATVKEAGRSIHEIPREEL-----RHTPELP	418
Query	1372	QSTRPIIEGSISQGTPIKFDNNSGQSAIK-HNVKSLITGPSKLSRGMPPLEIVPENIKVV	1430
		+ RP+ EGSI+QGT+K+D + + K H+V+SLI P + + PL+++ + + +	
Sbjct	419	LAPRPLKEGSITQGTPLKYDTGASTTGSKKHDVRSLIGSPGRTFPPVHPLDVMAD-ARAL	477
Query	1431	ERGKYEDVKAGETVRSRHTSVVSSGSPVLRST---LHEAPKAQLSPGIYDDTSARRTPV	1487
		ER YE E+++SR + SSG S+ R + E K + SP Y+D A	
Sbjct	478	ERACYE-----ESLKS RPGTASSSGGSIARGAPVIVPELGKPRQSPLTYEDHGA-----P	527
Query	1488	YQNTMSRGSPMMNRT-----SDVTISSNKSTNHERKSTLTPTQRESIPAKSPVPGVDPVV	1542
		+ + RGSP+ R + ++SS+K++ +RK T TP + AKSP V	
Sbjct	528	FAGHLPRGSPVTMREPTPRLQEGSLSSSKASQ-DRKLTSTPREI----AKSPHSTVPEHH	582
Query	1543	SH--SPFDPHHRGSTAGEVYRSHLPHTHLD-AMPFHRLDPAAAAYLFQRQLSPTPGYPS	1599
		H SP++ RG + ++YRSH+P DP ++P LD AAAAY R L+P P YP	
Sbjct	583	PHPISPYEHLRLGVSGVDLYRSHIPLAFDPTSIPRGIPLD-AAAAYYLPRLAPNPTYPH	641
Query	1600	QYQLY-----AMENTRQTIILNDYITSQQMQVNL-----RPDVARGLSPREQPLGL	1644
		Y Y A+EN RQTI+NDYITSQQM N R D+ RGLSPRE L L	
Sbjct	642	LYPPYLIRGYPDTAALEN-RQTIINDYITSQQMHNTATAMAQRADMLRGLSPRESSLAL	700
Query	1645	PYPA-TRGIIDLTMNPPT-ILVPHPGGTSTPPMDRITYIPGTQITFPPRPYNSASMSPGH	1702
		Y A RGIIDL+ +P +LVP GT MDR+ Y+P F R ++S+ +SPG	
Sbjct	701	NYAAGPRGIIDLSQVPHLPVLVPPTPGTPATAMDRLAYLPTAPQPFSSR-HSSSPLSPGG	759
Query	1703	PTHLA---AAASAEREREREREKERERERER---IAAASSDL----YLRPGSEQPG-----	1746
		PTHL +S+ERER+R+RE++R+RER I +++ + RPG+EQ	
Sbjct	760	PTHLTKPTTTSSSERERDRDRERDRDREREKSILTSTTTVEHAPIWRPGTEQSSGSSGSS	819
Query	1747	-----RPGSHGYVRSPSP-SVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMP	1797
		RP SH + SP S RTQ+ LQQRPSV T +IT ++P+ +	
Sbjct	820	GGGGGSSSRPASHSHAHQHSPISPRTQDA-LQQRPSVLHNTGMKGIITAVEPSKPTVLRS	878
Query	1798	LPAGGPSISQGLPASRYNTAADA-LAALVDAASAPQMDVSKTKESKHEAARLEENLRSR	1856
		P PA+ + A L +D V KE+ A	
Sbjct	879	TSTSSPV----RPAATFPPATHCPLGGTLDGVYPTLMEPVLLPKEAPRVAR-----	925
Query	1857	SAAVSEQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYE	1916
		E+ + + + K + ++ PS +P V PP S +	
Sbjct	926	----PERPRADTGHAFKAPPARSGLEPASSPSKGSEPRPLV-----PPVSGHA	970
Query	1917	EELRTRGKTTITAANFIDVIITRQIASDKDARERGSQSSDSS-----SSLSSHRYETPS	1970
		RT K A + AS D +QS S SL H	
Sbjct	971	TIARTPAKNL--APHHASPDPPAPPASASDPHREKTQSKPFSIQELELRSLGYHGSSYSP	1028
Query	1971	DAIEVISPASSPAPPQEKLTQYQPEVVKANQAENDPTRQYEGP-----LHHYRP--	2019
		+ +E +SP SSP+ +K E + + E + + GP L H RP	

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Sbjct  1029  EGVEPVSPVSSPSLTHDKGLPKHLEELDKSHLEGELRPKQPGPVKLGGEAAHLPHLRPLP  1088
Query  2020  -QQESPSPQQQLPPSSQAEGMGQVPRTHRLITLADHICQIITQDFARNQVSS-QTPQQPP  2077
          Q S SP Q P +                      R++TLA HI ++ITQD+ R+          P P
Sbjct  1089  ESQPSSSPLLQTAPGVKGH-----QRVVTLAQHISEVITQDYTRHHPQQLSAPLPAP  1140
Query  2078  TSTFQNSPSALVSTPVRTKTSNRYSPESQAQSVHHQRPGRSVSPENLVDKSRGSRPGKSP  2137
          +F + ++ +R S+ Y P                      H P +R SP          S G + P
Sbjct  1141  LYSFPGASCPVLD--LRRPPSDLYLPPPD-----HGAP-ARGSPH-----SEGGKRSPEP  1187
Query  2138  ERSHV---SSEPYEPISPPQ--VPVVEHKQDSLILLSQGAEPAEQRNDARSPGSISYLP  2192
          ++ V + EP+SPP+                      H + LL + G + R ++SPG+ S P
Sbjct  1188  NKTSVLGGGEDGIEPVSPPEGMTPEPHSRSAPVPLLYRDGEQTEPSRMGSKSPGNTSQPP  1247
Query  2193  SFFTCL-ENTSPMVKSKKQEIFRKLNSSGGGSDMAAAQPGTEIFNLPAVTTSGSVSSRG  2251
          +FF+KL E+ S MVKSKKQEI +KLN+ + + +QPGTEIFN+PA+T +G ++ R
Sbjct  1248  AFFSKLTESNSAMVKSQKQEIINKKLNTHNRNEPEYNISQPGTEIFNMPAITGTGLMTYRS  1307
Query  2252  HSFADPAS-NLGLEDIIRKALMGSFDDKVEDHGVVMS--QPMGVVPGTANTSVVTSGETR  2308
          + + AS N+GLE IIRKALMG +D E + + P+                      +T+ + R
Sbjct  1308  QAVQEHA STMGLEAIIRKALMGKYDQWEESPPLSANAFNPLNASASLPAAMPITAADGR  1367
Query  2309  REEGDPSPHSGGVCKPKLISKNSRKS KSPIPGQYLGTERPSSVSSVHSEGDYHRQTP-  2367
          + SP GG K K+ + +SRK+KSP P G +RP SVSSVHSEGD +R+TP
Sbjct  1368  SDHTLTSPGGG--KAKVSGRPSSRKAKSPAP--GLASGDRPPSVSSVHSEGDCNRRTPL  1423
Query  2368  -GWAWEDRPSSSTGSTQFPYNPLTMRM---LSSTPPTPIACAPSAVNQAAPHQQNRIWERE  2423
          WEDRPSS GST FPNYPL MR+ + ++PP P A S A PH W+ E
Sbjct  1424  TNRVWEDRPSSAGSTPFPYNPLIMRLQAGVMASPPPPGLPAGSG-PLAGPH---HAWDEE  1479
Query  2424  PAPLLSAQYETLSDSD 2439
          P PLL +QYETLSDS+
Sbjct  1480  PKPLLCSQYETLSDSE 1495

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CPU time: 0.14 user secs. 0.01 sys. secs 0.15 total secs.

Lambda K H
0.308 0.126 0.355

Gapped

Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 35,614

Number of extensions: 21670

Number of successful extensions: 45

Number of sequences better than 10.0: 1

Number of HSP's gapped: 3

Number of HSP's successfully gapped: 1

Length of query: 2440

Length of database: 1,196,146,007

Length adjustment: 151

Effective length of query: 2289

Effective length of database: 1,196,145,856

Effective search space: 2737977864384
Effective search space used: 2737977864384
Neighboring words threshold: 9
X1: 16 (7.1 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 42 (21.7 bits)
S2: 87 (38.1 bits)